

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:10:24 ; Search time 68.88 Seconds
(without alignments)
570.768 Million cell updates/sec

Title: US-09-456-306-2
Perfect score: 2985
Sequence: 1 MAHSYAEQLIDTLEAGCKVR.....CGVGAMIDLARSINRINPTP 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 6790655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1713 | 57.4 | 580 | 2 | T34668 |
| 2 | 1317.5 | 44.1 | 572 | 2 | DEEPCPC |
| 3 | 1101 | 36.9 | 572 | 2 | D82984 |
| 4 | 902.5 | 30.2 | 574 | 2 | S01682 |
| 5 | 855 | 28.6 | 574 | 2 | G69769 |
| 6 | 744.5 | 24.9 | 590 | 2 | C83382 |
| 7 | 637 | 21.3 | 553 | 2 | D69162 |
| 8 | 586.5 | 19.6 | 591 | 2 | F64334 |
| 9 | 576 | 19.3 | 577 | 2 | C69059 |
| 10 | 567 | 19.0 | 621 | 2 | S75115 |
| 11 | 554.5 | 18.6 | 574 | 2 | B69644 |
| 12 | 549 | 18.4 | 585 | 2 | T11997 |
| 13 | 546 | 18.3 | 612 | 2 | A44857 |
| 14 | 533.5 | 17.9 | 585 | 2 | C70341 |
| 15 | 533.5 | 17.9 | 590 | 1 | S28920 |
| 16 | 533.5 | 17.9 | 590 | 1 | S73251 |
| 17 | 526 | 17.6 | 618 | 2 | F70855 |
| 18 | 523.5 | 17.5 | 562 | 1 | YCECIL |
| 19 | 517.5 | 17.3 | 579 | 2 | B44857 |
| 20 | 515 | 17.3 | 548 | 1 | YCEC |
| 21 | 513 | 17.2 | 552 | 2 | G69464 |
| 22 | 508 | 17.0 | 613 | 2 | T35828 |
| 23 | 503 | 16.9 | 625 | 2 | T45413 |
| 24 | 502.5 | 16.8 | 584 | 2 | B72362 |
| 25 | 497 | 16.6 | 575 | 2 | D69512 |
| 26 | 493 | 16.5 | 670 | 1 | YCMU |
| 27 | 490.5 | 16.4 | 548 | 1 | A82375 |
| 28 | 490 | 16.4 | 548 | 1 | D82634 |
| 29 | 486 | 16.3 | 562 | 2 | G75044 |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 482.5 | 16.2 | 681 | 2 | T07968 | acetolactate synth |
| 31 | 480 | 16.1 | 599 | 2 | S15004 | acetolactate synth |
| 32 | 480 | 16.1 | 655 | 2 | S17691 | acetolactate synth |
| 33 | 477 | 16.0 | 652 | 2 | S25838 | acetolactate synth |
| 34 | 464.5 | 15.6 | 621 | 2 | JCS164 | acetolactate synth |
| 35 | 461.5 | 15.5 | 681 | 2 | T08085 | acetolactate synth |
| 36 | 461 | 15.4 | 594 | 1 | A56684 | acetohydroxy acid |
| 37 | 461 | 15.4 | 626 | 1 | A46648 | acetolactate synth |
| 38 | 460 | 15.4 | 683 | 2 | T07941 | acetolactate synth |
| 39 | 457 | 15.3 | 683 | 2 | T07912 | acetolactate synth |
| 40 | 454 | 15.2 | 659 | 2 | S60056 | acetolactate synth |
| 41 | 454 | 15.2 | 664 | 1 | YCNM2 | acetolactate synth |
| 42 | 454 | 15.2 | 667 | 1 | YCNM1 | acetolactate synth |
| 43 | 451 | 15.1 | 638 | 2 | S22490 | acetolactate synth |
| 44 | 449 | 15.0 | 575 | 1 | S35138 | acetolactate synth |
| 45 | 447.5 | 15.0 | 601 | 2 | I40666 | acetolactate synth |

ALIGNMENTS

RESULT 1
T34668
pyruvate dehydrogenase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 31-Jan-2000
C:Accession: T34668
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rørdam, B.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21552
A:Accession: T34668
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-580 <SNU>
A:Cross-references: EMBL:AL034446; PIDN:CAA22389.1; GSPDB:GN00070; SCODEB:SC1A9.19
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC1A9.19
C:Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain

| Query Match | Score | DB 2 | Length | 580 |
|---|-------|--|--------|-----|
| Best Local Similarity | 57.4% | | | |
| Matches 331; Conservativity 92; Mismatches 149; Indels 4; Gaps 4; | | | | |
| QY | 6 | AEGLIDLEAGVKRITGLVGSLSNPVAVRO-SDEWYVHVNNEEAAAFAGAESLITG | 64 | |
| DB | 7 | AEQFVDILTRAGVERLYGVGDSLPVDAVRHSGIEVHVHRETAFAAGAEADITG | 66 | |
| QY | 65 | ELAVCAASGPGMTHLIGLYDSHRNGAKVALASHIPSOIGSTPQETHPELPECS | 124 | |
| DB | 67 | KLACAGSCGPGMHLINGLYDSHRNSAPVLAASOTPSSEICLGFQETHPELPECS | 126 | |
| QY | 125 | GYCEWVNGEGEGRILHNAIOSTMAGKSVVYIPGDIKEDAGDGTYSSTISGTPV | 184 | |
| DB | 127 | HYSELLSPKQMRLLIOTAIHNAVGGGVSVSLPGDIAPRQGAETALVTS-RPTV | 185 | |
| QY | 185 | FPPPTFAALVEALINNAKSTYLCGAGVKARQVLEAEKISPIGHALGQYIOHEN | 244 | |
| DB | 186 | RPDDEEDRLVRMIDDAKVTLCGSGTACGANAHEVFEAKKLARVONALRGKEFIQYDN | 245 | |
| QY | 245 | PRFVGSGLIGVAGVDASNEADLLILGDPFYSPLRPD-NVAQVDICAHIGRTTV | 303 | |
| DB | 246 | PYVGSGLIGVAGVAYEATHECDLLIGDPFYNALPDQVKAQIDVPRHIGRSKL | 305 | |
| QY | 304 | KYPVTGDAVTINILPRVKEKTRDSFLDRMLKAHERKLSVVEYVHNNEKVPRIPEY | 363 | |
| DB | 306 | DLAVMGDARETLRCLIPRVKEKNRRRLDMKKHADLGCVKATYRKDKVPIHPEY | 365 | |
| QY | 364 | VASILELADKDAVFYVDGKCVNVAHARYTENBEGTRDVGSRHGTMANALPHAIQAS | 423 | |
| DB | 366 | VAALEMDADDAAVFPYVDGKCVNVAHARYT-SNGRRRIIGSFSGHGMANALPHAIQAO | 424 | |

424 VDRNRVIAACGCGGGLGMLLIGELLIVKQLPLKAVFNNSLGMVLEMLVEGQPEFGT 483
 425 TDRRQVVSMSGSGGFTLMQHDLPYKIVLFNNSSLGVELEMLVAGLPSHG 484
 484 DHEEVFAELIAAAGIKSVRIIDPKKVRQDLAALAYPGPVLDIYTDNALSTIPPTTW 543
 485 ANNPFAVAAEACGAFGVKVERKDLAAGALAAFKHKGKPALVDVTDNALSTIPKISA 544
 544 EOVMGFSKATRTVFGGVCAMIDLARSNIRNIPRP 579
 545 DMVTGALASRKIVLDGGVGRMLQMARSLNRNRP 580
 RESULT 2
 DEPCPC
 pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli
 N.Alternate names: pyruvate oxidase
 C.Species: Escherichia coli
 C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 05-Nov-1999
 C.Accession: A23648; G64825; I55291; I57856
 R.Grabau, C.; Cronan Jr., J.E.
 Nucleic Acids Res. 14, 5449-5460, 1986
 A.Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate
 A.Reference number: A23648; MUID:86286555
 A.Accession: A23648
 A.Molecule type: DNA
 A.Residues: 1-572 <GRA>
 A.Cross-references: GB:X04105; GB:M13947; GB:M13948; NID:9424272; PIDN:CAA27725.1; PID:94
 A.Experimental source: strain K-12
 R.Büttner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 S.ence, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A.Title: The complete genome sequence of Escherichia coli K-12.
 A.Reference number: A64720; MUID:97426617
 A.Accession: G64825
 A.Status: nucleic acid sequence not shown; translation not shown
 A.Molecule type: DNA
 A.Residues: 1-572 <BLAV>
 A.Cross-references: GB:AE000188; GB:U00096; NID:91787084; PIDN:AAC73958.1; PID:91787096;
 A.Experimental source: strain K-12, substrain MG1655
 R.Grabau, C.; Chang, Y.Y.; Cronan, J.E.
 J. Biol. Chem. 264, 12510-12519, 1989
 A.Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera
 A.Reference number: I55291; MUID:89308683
 A.Accession: I55291
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-363, 'HE', 366-413, 'HGV', 417-572 <RES>
 A.Cross-references: GB:M28208; NID:91009024; PIDN:AAB59101.1; PID:91009025
 A.Experimental source: strain K-12
 R.Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.
 Mol. Microbiol. 11, 1019-1028, 1994
 A.Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac
 A.Reference number: I57856; MUID:94293772
 A.Accession: I57856
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-22 <RE2>
 A.Cross-references: GB:S73268; NID:9685127; PIDN:AAB31180.1; PID:9685128
 C.Comment: The sequence of this protein was shown to be homologous with those of the lar
 ough pyruvate is the end product.
 C.Comment: This protein is not to be confused with a similar enzyme, pyruvate (or pyruv)
 ion of pyruvate to acetyl phosphate, carbon dioxide, and hydrogen peroxide.
 C.Genetics:
 A:Gene: poxB
 A:Map position: 19 min
 C:Complex: homotetramer
 C:Function:
 A:Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the
 A:Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of
 C:Superfamily: acetoacetate synthase large chain; thiamin pyrophosphate-binding domain
 C:Keywords: PBD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein
 F:422-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

F:50/Active site: Glu #status predicted

Query Match 44.1%; Score 1317.5; DB 1; Length 572;
 Best Local Similarity 46.3%; Pred. No. 1,3e-78;
 Matches 266; Conservative 106; Mismatches 195; Indels 7; Gaps 6;
 1 MAHSAEOLIDLEAGVKKRIYGLYSDSLNPIYDVAV-RQSDIEWHVYANEEAFAAAGAE 59
 1 MCOTAAATIAKLESAGVKRIWGTGSDLSLNGSLDLSLNRGTIEMWSTHHEEVAFAAAGAE 60
 60 SLITGELAVCAACGPGNTHLQGLYDSHRNCAKVALIASHIPSAQISTFPOETHPTIL 119
 61 AQLSELAVCAACGPGNTHLQGLYDSHRNCAKVALIASHIPSAQISTFPOETHPTIL 120
 120 FRECGTCBMYNGGQGERILHHAIOSTMAAGVSVVVPDIAKEDAGDGTYSNSTISS 179
 121 FRECHYCELVSPQIIOVALIAARKAVLNKGVSVVVPDIALKPAPEGA-TMHWYHA 179
 180 GTPVVEPPTFAALVEAIAINNAKSVTLPCGAGVKNARAOVLELAETKISPTGHALGQY 239
 180 POPVTPPEEBELKLAQLRYSNIALMCGSGCAGAKHELVFAGKIKAPTVHALRKEH 239
 240 IOHENPEVGNISGLYGACVDASNEADLLILGTFPYSDFLPKD-NVAQVDINGAHIG 298
 240 VEYDNPVDVGMTGLIGFSSGFHTMMNADTVLLGTFPYSDFLPKD-NVAQVDINGAHIG 299
 299 RTTYKYVTVGDVAATINILPHYKEKTRDSFLDMKKAHERKLSVVEYTHNVEKHVP 358
 300 AHSKVDMAVLDIKSTLALLPLVEEKADRFELDKALEDY-RDARKGIDDLAKPSEK--A 356
 359 IHPEVVASILNELDKDAVFTVDGMCNWHARYIENDEGRDPSRRHGTMANALPHA 418
 357 IHPQIAQIISHFPAADDAIFCDVGTPTWPAKRLK-MNGRRLLGSPNHSKMANAPQA 415
 419 TGAOSVDRNRVIAACGCGGGLGMLLIGELLIVKQLPLKAVFNNSLGMVLEMLVEGQ 478
 416 LGAQTEBERQVAVMGCGGSGFMSLMGDELVSQKPLKIVFNNSVLGFAVAMKMGY 475
 479 PEFGDHEEVFAELIAAAGIKSVRIIDPKKVRQDLAALAYPGPVLDIYTDNALSTIP 538
 476 LTFDGTEHDINIFARIAECGILTIGIRERKASEVDALRAESIDGPVLADVVAKEELAI 535
 539 PTITWEGMGFSKATRTVFGGVCAMIDLARSN 572
 536 PQILDEQAKGSLYMLAIRIISGRDEVIELAKTN 569
 RESULT 3
 D82984
 pyruvate dehydrogenase (cytochrome) PA5297 [imported] - Pseudomonas aeruginosa (strai
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: D82984
 C.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 Nature 406, 959-964, 2000
 A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950
 A:Accession: D82984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <STO>
 A.Cross-references: GB:AE004942; GB:AE004091; NID:99951607; PIDN:AA08682.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: poxB; PA5297
 Query Match 36.9%; Score 1101; DB 2; Length 572;
 Best Local Similarity 40.6%; Pred. No. 1,9e-64;
 Matches 226; Conservative 116; Mismatches 208; Indels 6; Gaps 4;

RESULT 6
C83382
probable decarboxylase PA2108 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
C:Accession: C83382
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Berry
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbidg, K.; Lim,
J.; Lory, S.; Olson, M.V.
N:Figure 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950
A:Accession: C83382
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1,590 <SMO>
A:Cross-references: GB:AE004638; GB:AE004091; NID:99948116; PIDN:AG05496.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
C:Gene: PA2108

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Query Match      21.3%; Score 637; Db 2; Length 553;
Best Local Similarity 30.4%; Pred. No. 41e-34;
Matches 164; Conservative 95; Mismatches 224; Indels 56; Gaps 6;

QY      6 AEOIDLTLEAGGVKRIYGLVGDLSLNPIDVAVRGSD-TEWYHVRNEEAAPAAAGESLITG 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      55 SEVFISQLAAGLTKYVFEGIPGSTFTLGLVDALRRNDEIRIYQVREHAAAFWASSYGLTGL 114

QY      65 ELAVCAASCGGNHLLIOGLYDSHRNGAKVYLAATSHPSAIOIGSTFQETHPELFECS 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      115 QPACMAVAGRAASNLITGLTDLDAALDRAPVLAVGHVEYTRIGTGAQSEIDHSLFSEFS 174

QY      125 GYCEMVNAGGEGERILLHAIIOSTWAGKGVSVVYRGDIAMEDADDGYNSTLSGGPV- 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 VYNNMTLVSPDEAAALAEAVKHAILERGVSHVDVPRVY-----QTMECTAPVK 222

QY      184 -----VFPDPTEAALVFEAINNAKSVTLFCGAGVKNARAQVLELAEKIPIGHA 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      223 PLRGMAEAATVPRPNRLRAADLINAEFRVYIAGGALEADSVYELAEFRIGALVST 262

QY      234 LGGQYIQLHNEPFEVGVSGSLGIGACYDASNEADLLILGTDPYSDFLPKDVAQYDIN 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      283 FRGKGIVDNDYPRYLICGHGSLGSAAAAEAVRKADLLVLTGSSFEDTLRIPPRRLIQYDID 342

QY      294 GAHIGRTVYKYPRTGVVAATIEMLPHVKEKIDRSLDKMLAKHNEKISSVYETTHNV 353
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      343 PMAVARHNHPVQGLTGSSLLVQELLISMWEEKEGPRFLAELGELRDMGLLSEADPSL 402

```


OY 476 EGOPEFGTTH--EEVNFADIAAAGIKSVRTDPKKVREQLAEALVPGPVLIDVTDPN 533
DB 479 FYDERMSHLEVPDFVLAESFVEAREIEEPGETSEALSRAIRKSGPALLIDYDPD 538
OY 534 AL--SIPPTITWEQVWG 548
DB 539 EILPMVPGCGLTETVIG 555

RESULT 10
S75115
acetylcholine synthase - *Synechocystis* sp. (strain PCC 6803)

N:Alternate names: protein sir2088

C:Species: *Synechocystis* sp.

A:Accession: PCC 6803

C:Date: 25-Apr-1997

C:Accession: S75115

C:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

A:Reference number: S74322; MUID:97061201

A:Accession: S75115

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-621 <KAN>

A:Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17977.1; PID:g165306

A:Notes: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: *llvG*

A:Start codon: GTG

C:Superfamily: acetylcholine synthase large chain; thiamin pyrophosphate-binding domain

Query Match 19.0%; Score 567; DB 2: Length 621;
Best Local Similarity 27.4%; Pred. No. 1.8e-29;
Matches 164; Conservative 113; Mismatches 236; Indels 86; Gaps 18;

OY 9 LIDTLEAGVKKRIYGLVDSLNPIYDAVRO---SDIEVWHRNEEAAFAAGASLITG 64
DB 27 LMDSLKRGVKKHIFPGALIPYDELRYFAAGEIHLVHRHOGSHADGAKRATG 86
OY 65 ELAVCAASGPGENTHLLIOGLYDSHRNGAKVLAISHIPSAIGSTFFOE-----THPEI 118
DB 87 KVGVEGSGPGATNLVGINAHLDVPMVYITGVGRAMIGSDAFQEIIDFITLPIV 146
OY 119 LKEGSGVCEWNGEGEGRILHNAIIOSTMAGK-GVSVVVIIPGDLAKE-----DADGG 170
DB 147 -----KSHYVRSADMARITTEAFHILASTGRPEVILIDIPKDVGLDECEYIPLDPGD- 199
OY 171 TYSNSTISSGTPVPPDETEAAALVEAINNAKSVTLFCGAG--VKNARQVLELAETIKS 228
DB 200 ---VNLPGYRPTVYKGNROINAAQLLEQARNPLLYGGGAIANNAHQVFAERERQL 255
OY 229 PIGHALGKQYIQHNPPEVGMSCILGYACVDASNEADLLILGLTDF-----PYSDFL 282
DB 256 PVTTLIMIGAFDENHPSVGMIGMGTAVANFVSECDLLIAGVAREDDRVTKLDEFA 315
OY 283 PKDVAOVDINGAHIGRTYKPYTGDVANTENILPHYKE-----KIDRSLEDMKL 335
DB 316 SRAKVIHIDIDAEVGNRRADPVPVGVRRVRLQLQRAEELDYPTHPPTTQALNR-- 373
OY 336 KAHREKLSSVETVTHNEKIVPIHPEYVA--STINELADK--DAVFTVDTGKCVNHAR 391
DB 374 -----IDHWRITDPLVPHEDTIAPOEVVHEIGRARPARYITTTDVGQOMMAAQ 423
OY 392 YIENPEGRDFVGSFRGTMANALPHATGAOSVDRNRQVLAACDGGIGMLIGELTVKL 451
DB 424 FLNN--GFRRWISSAGLGTGFLPAAMGAKVGVGDEAVICISDASFOHMLQELGLTAQ 481
OY 452 HQLLKAVVFNSSIGCWK-----LEMLVSGQPEFGTIDHEVNFALIAAAGT 499

DB 482 YDIQVKTILLNMGWGNVROMOOFYEEERYSAKNSQGM-----DINL--LCEAYGI 532
OY 500 KSVRTDPKKVREQLAEALVPGPVLIDYV--DPNAL-SIPPTITWEQVWGFSKATR 555
DB 533 KGIYRKREDLAPALAEMLAHNGPVMVAVKKNDCYPMIAPGKSNOMLGLTEPEVR 591

RESULT 11
B69644

acetylcholine synthase (EC 4.1.3.18) large chain - *Bacillus subtilis*

C:Species: *Bacillus subtilis*

C:Date: 05-Dec-1997

C:Accession: B69644; 139865

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azecvedo, V.; Ber

C:Broon, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A:Enrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbry, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.

leach, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hu

koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; L

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma

Y. M.; Ogawa, K.; Ogikawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Port

Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scari

A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zunshtein, E.; Yoshikawa, H.; Dancho, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*

A:Reference number: B69580; MUID:98044033

A:Accession: B69644

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-574 <KUN>

A:Cross-references: GB:299118; GB:AL009126; NID:g2635200; PIDN:CAB14791.1; PID:g26352

A:Experimental source: strain 168

R:Grandoni, J.A.; Zahler, S.A.; Galvo, J.M.

J. Bacteriol. 174, 3212-3219, 1992

A:Title: transcriptional regulation of the *llv*-*leu* operon of *Bacillus subtilis*.

A:Reference number: 139865; MUID:92250415

A:Accession: 139865

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-20, 'R' <RES>

A:Cross-references: GB:M87009; NID:g143096; PIDN:AAA22550.1; PID:g143097

C:Genetics:

A:Gene: *llvB*

C:Superfamily: acetylcholine synthase large chain; thiamin pyrophosphate-binding

C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein

F;443-491/Domain: thiamin pyrophosphate-binding domain homology <TPB>

F;64/Active site: Glu #status predicted

Query Match 18.6%; Score 554.5; DB 2: Length 574;
Best Local Similarity 28.7%; Pred. No. 1.1e-28;
Matches 154; Conservative 113; Mismatches 251; Indels 19; Gaps 9;

OY 4 SYAQLIDTLEAGVKKRIYGLVDSLNPIYDAVROSDIEVWHRNEEAAFAAGASLITG 63
DB 19 SGALMLIESLKEKEVEMIFPGGAVIPYDKLYNSGLVILHRRHGGALHAAEGVARVS 78
OY 64 GELAVCAASGPGENTHLLIOGLYDSHRNGAKVLAISHIPSAIGSTFFOEITHPEIIFKEC 123
DB 79 GKPGVVATISGPGATNLVGTGLADAMISLPLVFTGVAVSVISGDAFGADLLGITMPV 138
OY 124 SGCEWYNGEGEGRILHNAIIOSTMAGK-GVSVVVIIPGDLAKEADGDTYNSSTISSG-T 181
DB 139 TKHSYQVROPEDPRLRIKEAFPHIATGRPGPVLIDIPKDVATTE-GRFSYDHMMNLPQYQ 197
OY 182 PVVPPDTEAAALVEAINNAKSVTLFCGAGVKNARA--QVLELAETIKSPIGHALGKQY 239
DB 198 PTEPNLQIRKLEAVNAASKKPYIILAGAGVLHGKASEELKNVAEQQILPVATHTLLGLG 257
OY 240 IOHENPFEVGMSCILGYACVDASNEADLLILGLTDF-----YSDFLPKDVAQVDIN 293

Db 258 FRADHPLFGMAGMCHGCTYTAANMALHCECDLISIGARDDEVTGNLKHFAANNAIAHDIID 317
OY 294 GAHIGRTTYKYPVTDGVAATENILPHYKEKIDRSFLDMMLKAHERKLSVETITHY 353
Db 318 PAETGIMKTQIPVVDSDKIVLDELKODKOSDSEMKKOLEMKEEYPL--WYVDNE 374
OY 354 EKHVPIHPEYVASILNELADKDAVFTVDTQMCNVMHARYIENPEGRDEFGVSPRHGTMAN 413
Db 375 EE--GFKPQKLEYIHQFTKGALVATDVQGHQMSAQFPPQKADK--WYSSGGLTGMF 431
OY 414 ALPHAIQAQSVDRNRQVIAMCGDGLMGLGELLTYKHLQPLKAVVFNNSIGMWK--L 471
Db 432 GLPAAIGAQAIEKDAIVAVAVGCGFQMTLQELDVIREMLPVKVVILNACGVMRWQ 491
OY 472 EMVEGQPEFGTDEHEVNFPAEIAAGIKSVRTIDPKKVEQALAPGVLIDT 528
Db 492 EIFYERYSKSPASQDPVKLSAEAYIKGIRISSEAEKLEALTSREPVVIDV 548

RESULT 12

T11997
acetylhydroxyacid synthase large subunit - red alga (Cyanidium caldarium) chloroplast
C:Species: Chloroplast Cyanidium caldarium
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C:Accession: T11997
R:Gloeckner, G.; Rosenthal, A.; Valentin, K.
submitted to the EMBL Data Library, September 1997
A:Description: Organization of 46 kb of the Cyanidium caldarium RKL plastid genome.
A:Reference number: Z17374
A:Accession: T11997
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-585 <GLOS>
A:Cross-references: EMBL:AF022186; NID:92465730; PIDN:AAB82660.1; PID:92465731
A:Experimental source: strain RKL
C:Genetics:
A:Genome: chloroplast
A:Note: 11VB
C:Superfamily: acetylacetyl synthase large chain; thiamin pyrophosphate-binding domain
C:Keywords: chloroplast
F:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.4%; Score 549; DB 2; Length 585;
Best Local Similarity 27.3%; Pred. No. 2.5e-28;

Matches 160; Conservative 112; Mismatches 247; Indels 68; Gaps 15;

OY 9 LIDTLEAGGVKRIYGLVGSLSNPIDVAV---RQSDIEWVHVRNEEAFAAGAESLITG 64
Db 16 LIDMLVKIHKVNIIFGVRGAILRITVDELYHMEKKLIKINYLVRHESAAHAAVAVRATN 75
OY 65 ELAVCAASGCGPNTILIOGLYDSHRNGAKVLAISHIPSAQISTGFTFOETHPILREKES 124
Db 76 EGVGVCLATGCPGATNLVTGATPAQMDSPRIATIGQVSRFAETGTDFAFOEJDIETPLTV 135
OY 125 GCEVNGEAGEGGRILHNIQSTMAK--GVSVVYIPGDIADKEDAG---DGTSSNSTISS 179
Db 136 KHSFVRDRPDISTIVSEAFYISKGRPRGAVLIDPKDGLFEFNHNDISIDHPIIK 195
OY 180 GTPVVPDPTEAALVEAIAINNAKSVTLFCGAGVAKNAAQ--VLELAEKIKSPIGHALGK 237
Db 196 YRTIVGPRSRQIEKFKMLLESKOPILYVGAGVMSRAKHETIELASFIKIPVTTLMGK 255
OY 238 QYIQHNEPFEVHSGGLGACVDASNEADLLILGTDG-----PYSDFLPDQNAQVD 291
Db 256 GSFNEVNPYULGIMGHGTAAYANFAVSECDLLITAGARFDRVYTGKLDSEACNAQVIVHD 315
OY 292 INGAUIGRTTYKYPVTDGVAATENILPHVKEKIDRSFLDMMLKAHERKLSVETITHY 351
Db 316 IDPAETGKRIIPQALIIISDIKIVLEKLSMKEGTNN--MDK-----NOTQAMHL 363
OY 352 NVEK-----HVP-----IHPEYVASILNELADKDAVFTVDTQMCNVMHARYIENPEGT 399

Db 364 RIHKWKEYPLSIPHSKLLYPQEVINEISQIAQK-AFFATVDVQGHQMSAQFELKVEGQ- 421
OY 400 RDEVGSRRHCTMNAALPHAIQAQSVDRNRQVIAMCGGGGGLMGLGELLTYKHLQPLKAV 459
Db 422 -KWLSSGSLTGMVGLPAAIGAKIANPNDLICITDGASFOYMLQELGTIAOYELDIKIF 480
OY 460 VFNNSISGMVKL-----EMVEGQPEFGTDEHEVNFPAEIAAGIKSVRTIDP 507
Db 481 IINNQGVNVRWQQAIFEDRYAHSNNAKQPD-----FVQLANSIGIKIRTTSS 531
OY 508 KKVREQLAEALAPGVLID--IVTDPNAL--SIPTITWQVYGFSK 551
Db 532 KDLKSRIERTISPPGILLIDICVATSENCYPMIAPKSNQSMGLTK 578

RESULT 13

A44857
acetylacetyl synthase (EC 4.1.3.18) - Spirulina platensis
C:Species: Spirulina platensis
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Oct-1999
C:Accession: A44857
R:Milano, A.; De Rossi, E.; Zanaria, E.; Barbierato, L.; Clifert, O.; Riccardi
J. Gen. Microbiol. 138, 1399-1408, 1992
A:Title: Molecular characterization of the genes encoding acetylhydroxy acid synthase
A:Reference number: A44857; NUID:92381487
A:Accession: A44857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-612 <MLD>
A:Note: sequence extracted from NCBI backbone (NCBI:112275, NCBI:112276)
C:Superfamily: acetylacetyl synthase large chain; thiamin pyrophosphate-binding domain
C:Keywords: branched-chain amino acid biosynthesis; carbon carbon lyase; oxo-acid-lyase
F:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.3%; Score 546; DB 2; Length 612;
Best Local Similarity 26.6%; Pred. No. 4.2e-28;

Matches 164; Conservative 123; Mismatches 253; Indels 76; Gaps 19;

OY 6 AEDLITLEAGGVKRIYGLVGSLSNPIDVAV---AVRQSDIEWVHVRNEEAFAAGAESL 61
Db 15 AFRILDSLKRNGVONIFGVRGAILRITVDELYHMEKKLIKINYLVRHESAAHAAVAVRATN 74
OY 62 INGEVLCAASGCGPNTILIOGLYDSHRNGAKVLAISHIPSAQISTGFTFOETHPILREKES 114
Db 75 ATGRVGVCEGTSGPATNLVTGATPAQMDSPRIATIGQVSRFAETGTDFAFOEJDIETPLTV 134
OY 115 ---HPEILFEKESGCEVNGEAGE--RILHNAIQTMAK--GVSVVYIPGDIADKED- 166
Db 135 PIYKHSYV-----REGRDMATVADAHIASTGPRPVILIDVPRDGLIEF 181
OY 167 ---AGDGYVSNSTISSGTPVVPDPTEAALVEAIAINNAKSVTLFCGAGV--KNARQVL 220
Db 182 DYIVNPGEVS--LRGVRTVKGAVRQIQAILEABERPLMYVGGAISATPAHEIA 238
OY 221 ELAEKIKSPIGHALGKQYIQHNEPFEVHSGGLGACVDASNEADLLILGTDG----- 276
Db 239 ELAELEFQIPVTTLMKGSFDEKRNPLSYGLMIGHGTAAYANFAVSECDLLITAGARFDRV 298
OY 277 --PYSDFLPDQNAQVDINGANIGRTTYKYPVTDGVAATENILPHVKEKIDRSFLDMMLKA 327
Db 299 TGRLDSEFGSAKYNIIIDIPAEVGNKRTPEVPIVGDVQVYLHLLRCRGTIGVGNQNT 358
OY 328 RSEFLDMMLKAHERKLSVETITHYHNEKIVPIHPEYVASILNELADKDAVFTVDTQMCNV 387
Db 359 OSWLEIRINRPE--DYPLVVPYSDS-----LAPQVYIAELGMA--PDGYTTVDVQGHQ 410
OY 388 WHARTYIENPEGTDFVGSFRHGTMANALPHAIQAQSVDRNRQVIAMCGGGGGLMGLGELL 447
Db 411 WAAQFLKN--GPRQWISAGLGTMGYGISPMAGKVALERSQVCIAGDASVQMNIOELG 468
OY 448 TVKHLQPLKAVVFNNSISGMVKLEMLVEGQPEFGTDEHEV--NPAETIAAAGIKSVRI 504

Mon Mar 19 12:21:50 2001

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Job time: 2596 sec

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